

# SEQUENCE LISTING

<110> Duprat, Fabrice  
Lesage, Florian  
Fink, Michel  
Lazdunski, Michel

<120> FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS

<130> 1201-CIP-DIV-00

<141> 2001-08-24

<150> 09/144,914

<151> 1998-09-01

<150> 08/749,816

<151> 1996-11-15

<150> 60/095,234

<151> 1998-08-04

<150> FR 96/01565

<151> 1996-02-08

<160> 24

<170> PatentIn Ver. 2.0

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<222> (183)..(1190)

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Met Leu Gln Ser Leu Ala Gly Ser Ser Cys Val Arg Leu Val Glu

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5

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15

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Arg His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu

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Leu Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro

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Leu	Glu	Glu	His	Glu	Cys	Leu	Ser	Glu	Gln	Gln	Leu	Glu	Gln	Phe	Leu	
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ggc	cgg	gtg	ctg	gag	gcc	agc	aac	tac	ggc	gtg	tcg	gtg	ctc	agc	aac	467
Gly	Arg	Val	Leu	Glu	Ala	Ser	Asn	Tyr	Gly	Val	Ser	Val	Leu	Ser	Asn	
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Ala	Ser	Gly	Asn	Trp	Asn	Trp	Asp	Phe	Thr	Ser	Ala	Leu	Phe	Phe	Ala	
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Asp	Gly	Gly	Lys	Ala	Phe	Cys	Ile	Ile	Tyr	Ser	Val	Ile	Gly	Ile	Pro	
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Phe	Thr	Leu	Leu	Phe	Leu	Thr	Ala	Val	Val	Gln	Arg	Ile	Thr	Val	His	
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Val	Thr	Arg	Arg	Pro	Val	Leu	Tyr	Phe	His	Ile	Arg	Trp	Gly	Phe	Ser	
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Lys	Gln	Val	Val	Ala	Ile	Val	His	Ala	Val	Leu	Leu	Gly	Phe	Val	Thr	
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Asp	Asp	Trp	Asn	Phe	Leu	Glu	Ser	Phe	Tyr	Phe	Cys	Phe	Ile	Ser	Leu	
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Ser	Thr	Ile	Gly	Leu	Gly	Asp	Tyr	Val	Pro	Gly	Glu	Gly	Tyr	Asn	Gln	
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Lys	Phe	Arg	Glu	Leu	Tyr	Lys	Ile	Gly	Ile	Thr	Cys	Tyr	Leu	Leu	Leu	
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Gly	Leu	Ile	Ala	Met	Leu	Val	Val	Leu	Glu	Thr	Phe	Cys	Glu	Leu	His	
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Glu	Leu	Lys	Lys	Phe	Arg	Lys	Met	Phe	Tyr	Val	Lys	Lys	Asp	Lys	Asp	
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Glu Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser  
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atc aca gac cag gca gct ggc atg aaa gag gac cag aag caa aat gag 1139  
Ile Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu  
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cct ttt gtg gcc acc cag tca tct gcc tgc gtg gat ggc cct gca aac 1187  
Pro Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn  
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cat tgagcgtagg atttgttgca ttatgctaga gcaccagggt cagggtgcaa 1240  
His

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aagaaatagc tactgtttgc aatgtcttat taaaaaacia caaaaaaaga cacatggaac 1360

aaagaagctg tgaccccagc aggatgtcta atatgtgagg aaatgagatg tccacctaaa 1420

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Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro Tyr  
35 40 45

Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe Leu  
50 55 60

Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu Gly  
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Arg	Val	Leu	Glu	Ala	Ser	Asn	Tyr	Gly	Val	Ser	Val	Leu	Ser	Asn	Ala	
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Asp	Trp	Asn	Phe	Leu	Glu	Ser	Phe	Tyr	Phe	Cys	Phe	Ile	Ser	Leu	Ser	
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Leu	Ile	Ala	Met	Leu	Val	Val	Leu	Glu	Thr	Phe	Cys	Glu	Leu	His	Glu	
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Thr	Asp	Gln	Ala	Ala	Gly	Met	Lys	Glu	Asp	Gln	Lys	Gln	Asn	Glu	Pro	
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ggacg atg aag cgg cag aac gtg cgc acg ctg gcg ctc atc gtg tgc acc 170
    Met Lys Arg Gln Asn Val Arg Thr Leu Ala Leu Ile Val Cys Thr
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ttc acc tac ctg ctg gtg ggc gcc gcg gtc ttc gac gcg ctg gag tgc 218
Phe Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser
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gag ccc gag ctg atc gag cgg cag cgg ctg gag ctg cgg cag cag gag 266
Glu Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu
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ctg cgg gcg cgc tac aac ctc agc cag ggc ggc tac gag gag ctg gag 314
Leu Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu
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cgc gtc gtg ctg cgc ctc aag ccg cac aag gcc ggc gtg cag tgg cgc 362
Arg Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg
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Phe Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly
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tac ggg cac gcg gca ccc agc acg gat ggc ggc aag gtg ttc tgc atg 458
Tyr Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met
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ttc tac gcg ctg ctg ggc atc ccg ctc acg ctc gtc atg ttc cag agc 506
Phe Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser
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ctg ggc gag cgc atc aac acc ttg gtg agg tac ctg ctg cac cgc gcc 554
Leu Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala
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aag aag ggg ctg ggc atg cgg cgc gcc gac gtg tcc atg gcc aac atg 602
Lys Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met
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gtg ctc atc ggc ttc ttc tcg tgc atc agc acg ctg tgc atc ggc gcc 650
Val Leu Ile Gly Phe Phe Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala
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gcc gcc ttc tcc cac tac gag cac tgg acc ttc ttc cag gcc tac tac 698
Ala Ala Phe Ser His Tyr Glu His Trp Thr Phe Phe Gln Ala Tyr Tyr
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tac tgc ttc atc acc ctc acc acc atc ggc ttc ggc gac tac gtg gcg 746
Tyr Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala
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ctg cag aag gac cag gcc ctg cag acg cag ccg cag tac gtg gcc ttc 794
Leu Gln Lys Asp Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe
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Asn Leu Val Val Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys	
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cgc gac gcc gag cac cgc gcg ctg ctc acg cgc aac ggg cag gcg ggc	938
Arg Asp Ala Glu His Arg Ala Leu Leu Thr Arg Asn Gly Gln Ala Gly	
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ggc ggc gga ggg ggt ggc agc gcg cac act acg gac acc gcc tca tcc	986
Gly Gly Gly Gly Gly Gly Ser Ala His Thr Thr Asp Thr Ala Ser Ser	
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acg gcg gca gcg ggc ggc ggc ggc ttc cgc aac gtc tac gcg gag gtg	1034
Thr Ala Ala Ala Gly Gly Gly Gly Phe Arg Asn Val Tyr Ala Glu Val	
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ctg cac ttc cag tcc atg tgc tgc tgc ctg tgg tac aag agc cgc gag	1082
Leu His Phe Gln Ser Met Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu	
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Lys Leu Gln Tyr Ser Ile Pro Met Ile Ile Pro Arg Asp Leu Ser Thr	
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Ser Asp Thr Cys Val Glu Gln Ser His Ser Ser Pro Gly Gly Gly Gly	
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Arg Tyr Ser Asp Thr Pro Ser Arg Arg Cys Leu Cys Ser Gly Ala Pro	
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cgc tcc gcc atc agc tgc gtg tcc acg ggt ctg cac agc ctg tcc acc	1274
Arg Ser Ala Ile Ser Ser Val Ser Thr Gly Leu His Ser Leu Ser Thr	
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Phe Arg Gly Leu Met Lys Arg Arg Ser Ser Val	
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<223> TASK

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Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu Leu  
 35 40 45

Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu Arg  
 50 55 60

Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe  
 65 70 75 80

Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr  
 85 90 95

Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe  
 100 105 110

Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu  
 115 120 125

Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala Lys  
 130 135 140

Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met Val

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Leu Ile Gly Phe	Phe Ser Cys Ile Ser	Thr Leu Cys Ile Gly	Ala Ala			
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Ala Phe Ser His	Tyr Glu His Trp Thr	Phe Phe Gln Ala	Tyr Tyr Tyr			
	180	185	190			
Cys Phe Ile Thr	Leu Thr Thr Ile Gly	Phe Gly Asp Tyr	Val Ala Leu			
	195	200	205			
Gln Lys Asp Gln	Ala Leu Gln Thr Gln	Pro Gln Tyr Val	Ala Phe Ser			
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Phe Val Tyr Ile	Leu Thr Gly Leu Thr	Val Ile Gly Ala	Phe Leu Asn			
	225	230	235			240
Leu Val Val Leu	Arg Phe Met Thr Met	Asn Ala Glu Asp	Glu Lys Arg			
	245	250	255			
Asp Ala Glu His	Arg Ala Leu Leu Thr	Arg Asn Gly Gln	Ala Gly Gly			
	260	265	270			
Gly Gly Gly Gly	Gly Ser Ala His Thr Thr	Asp Thr Ala Ser	Ser Thr			
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Ala Ala Ala Gly	Gly Gly Gly Phe Arg Asn	Val Tyr Ala Glu	Val Leu			
	290	295	300			
His Phe Gln Ser	Met Cys Ser Cys Leu Trp	Tyr Lys Ser Arg	Glu Lys			
	305	310	315	320		
Leu Gln Tyr Ser	Ile Pro Met Ile Ile	Pro Arg Asp Leu	Ser Thr Ser			
	325	330	335			
Asp Thr Cys Val	Glu Gln Ser His Ser	Ser Pro Gly Gly	Gly Gly Arg			
	340	345	350			
Tyr Ser Asp Thr	Pro Ser Arg Arg Cys	Leu Cys Ser Gly	Ala Pro Arg			
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 Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met



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 Tyr Asn Leu Ser Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu  
 50 55 60  
 Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser  
 65 70 75 80  
 Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala  
 85 90 95  
 Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu  
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 115 120 125  
 Ile Asn Thr Phe Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu  
 130 135 140  
 Gly Met Arg His Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly  
 145 150 155 160  
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 Tyr Tyr Glu Arg Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile  
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 Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp  
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 245 250 255  
 His Arg Ala Leu Leu Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly  
 260 265 270  
 Leu Ser Cys Leu Ser Gly Ser Leu Gly Asp Val Arg Pro Arg Asp Pro  
 275 280 285  
 Val Thr Cys Ala Ala Ala Ala Gly Gly Val Gly Val Gly Val Gly Gly  
 290 295 300  
 Ser Gly Phe Arg Asn Val Tyr Ala Glu Val Leu His Phe Gln Ser Met  
 305 310 315 320  
 Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu Lys Leu Gln Tyr Ser Ile  
 325 330 335  
 Pro Met Ile Ile Pro Arg Asp Leu Ser Thr Ser Asp Thr Cys Val Glu  
 340 345 350

His Ser His Ser Ser Pro Gly Gly Gly Gly Arg Tyr Ser Asp Thr Pro  
 355 360 365

Ser His Pro Cys Leu Cys Ser Gly Thr Gln Arg Ser Ala Ile Ser Ser  
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Arg Arg Ser Ser Val  
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 35 40 45

Phe Asn Leu Ile Gly Ala Gly Ile Phe Tyr Leu Ala Glu Thr Gln Asn  
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Ser Ser Glu Ser Leu Asn Glu Asn Ser Glu Val Ser Lys Cys Leu His  
 65 70 75 80

Asn Leu Pro Ile Gly Gly Lys Ile Thr Ala Glu Met Lys Ser Lys Leu  
 85 90 95

Gly Lys Cys Leu Thr Lys Ser Ser Arg Ile Asp Gly Phe Gly Lys Ala  
 100 105 110

Ile Phe Phe Ser Trp Thr Leu Tyr Ser Thr Val Gly Tyr Gly Ser Leu  
 115 120 125

Tyr Pro His Ser Thr Leu Gly Arg Tyr Leu Thr Ile Phe Tyr Ser Leu  
 130 135 140

Leu Met Ile Pro Val Phe Ile Ala Phe Lys Phe Glu Phe Gly Thr Phe  
 145 150 155 160

Leu Ala His Phe Leu Val Val Val Ser Asn Arg Thr Arg Leu Ala Val  
 165 170 175

Lys Lys Ala Tyr Tyr Lys Leu Ser Gln Asn Pro Glu Asn Ala Glu Thr  
 180 185 190

Pro Ser Asn Ser Leu Gln His Asp Tyr Leu Ile Phe Leu Ser Ser Leu  
 195 200 205

Leu Leu Cys Ser Ile Ser Leu Leu Ser Ser Ser Ala Leu Phe Ser Ser  
 210 215 220  
 Ile Glu Asn Ile Ser Tyr Leu Ser Ser Val Tyr Phe Gly Ile Ile Thr  
 225 230 235 240  
 Met Phe Leu Ile Gly Ile Gly Asp Ile Val Pro Thr Asn Leu Val Trp  
 245 250 255  
 Phe Ser Gly Tyr Cys Met Leu Phe Leu Ile Ser Asp Val Leu Ser Asn  
 260 265 270  
 Gln Ile Phe Tyr Phe Cys Gln Ala Arg Val Arg Tyr Phe Phe His Ile  
 275 280 285  
 Leu Ala Arg Lys Ile Leu Leu Leu Arg Glu Glu Asp Asp Gly Phe Gln  
 290 295 300  
 Leu Glu Thr Thr Val Ser Leu Gln His Ile Pro Ile Ile Asn Ser Gln  
 305 310 315 320  
 Cys Met Pro Ser Leu Val Leu Asp Cys Glu Lys Glu Glu Leu Asp Asn  
 325 330 335  
 Asp Glu Lys Leu Ile Ser Ser Leu Thr Ser Thr  
 340 345

<210> 7

<211> 383

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: TWIK-1 homolog

<400> 7

Met Thr Val Ser Met Glu Glu Asn Ser Lys Ile Gln Met Leu Ser Ala  
 1 5 10 15  
 Thr Ser Lys Asp Lys Lys Val Ala Thr Asp Arg Ser Leu Leu Asn Lys  
 20 25 30  
 Tyr His Leu Gly Pro Leu Ala Leu His Thr Gly Leu Val Leu Ser Cys  
 35 40 45  
 Val Thr Tyr Ala Leu Gly Gly Ala Tyr Leu Phe Leu Ser Ile Glu His  
 50 55 60  
 Pro Glu Glu Leu Lys Arg Arg Glu Lys Ala Ile Arg Glu Phe Gln Asp  
 65 70 75 80  
 Leu Lys Gln Gln Phe Met Gly Asn Ile Thr Ser Gly Ile Glu Asn Ser  
 85 90 95  
 Glu Gln Ser Ile Glu Ile Tyr Thr Lys Lys Leu Ile Leu Met Leu Glu  
 100 105 110  
 Asp Ala His Asn Ala His Ala Phe Glu Tyr Phe Phe Leu Asn His Glu  
 115 120 125

Ile	Pro	Lys	Asp	Met	Trp	Thr	Phe	Ser	Ser	Ala	Leu	Val	Phe	Thr	Thr		
130						135					140						
Thr	Thr	Val	Ile	Pro	Val	Gly	Tyr	Gly	Tyr	Ile	Phe	Pro	Val	Ser	Ala		
145					150					155					160		
Tyr	Gly	Arg	Met	Cys	Leu	Ile	Ala	Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu		
				165					170					175			
Thr	Leu	Val	Thr	Met	Ala	Asp	Thr	Gly	Lys	Phe	Ala	Ala	Gln	Leu	Val		
			180					185					190				
Thr	Arg	Trp	Phe	Gly	Asp	Asn	Asn	Met	Ala	Ile	Pro	Ala	Ala	Ile	Phe		
		195					200					205					
Val	Cys	Leu	Leu	Phe	Ala	Tyr	Pro	Leu	Val	Val	Gly	Phe	Ile	Leu	Cys		
	210					215					220						
Ser	Thr	Ser	Asn	Ile	Thr	Tyr	Leu	Asp	Ser	Val	Tyr	Phe	Ser	Leu	Thr		
225					230					235					240		
Ser	Ile	Phe	Thr	Ile	Gly	Phe	Gly	Asp	Leu	Thr	Pro	Asp	Met	Asn	Val		
				245					250					255			
Ile	His	Met	Val	Leu	Phe	Leu	Ala	Val	Gly	Val	Ile	Leu	Val	Thr	Ile		
			260					265					270				
Thr	Leu	Asp	Ile	Val	Ala	Ala	Glu	Met	Ile	Asp	Arg	Val	His	Tyr	Met		
		275					280					285					
Gly	Arg	His	Val	Gly	Lys	Ala	Lys	Glu	Leu	Ala	Gly	Lys	Met	Phe	Gln		
	290					295					300						
Leu	Ala	Gln	Ser	Leu	Asn	Met	Lys	Gln	Gly	Leu	Val	Ser	Gly	Val	Gly		
305					310					315					320		
Gln	Leu	His	Ala	Leu	Ala	Arg	Phe	Gly	Met	Leu	Val	Gly	Arg	Glu	Glu		
			325					330						335			
Val	Asp	Lys	Thr	Gln	Glu	Asp	Gly	Ile	Ile	Ala	Phe	Ser	Pro	Asp	Val		
			340					345					350				
Met	Asp	Gly	Leu	Glu	Phe	Met	Asp	Thr	Leu	Ser	Ile	Tyr	Ser	Arg	Arg		
		355					360					365					
Ser	Arg	Arg	Ser	Ala	Glu	Asn	Ser	Ala	Arg	Asn	Leu	Phe	Leu	Ser			
	370					375					380						

<210> 8  
 <211> 370  
 <212> PRT  
 <213> Murine

<220>  
 <223> TREK-1

<400>	8																
Met	Ala	Ala	Pro	Asp	Leu	Leu	Asp	Pro	Lys	Ser	Ala	Ala	Gln	Asn	Ser		
1				5					10					15			

Lys Pro Arg Leu Ser Phe Ser Ser Lys Pro Thr Val Leu Ala Ser Arg  
 20 25 30  
 Val Glu Ser Asp Ser Ala Ile Asn Val Met Lys Trp Lys Thr Val Ser  
 35 40 45  
 Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Ala Val  
 50 55 60  
 Phe Lys Ala Leu Glu Gln Pro Gln Glu Ile Ser Gln Arg Thr Thr Ile  
 65 70 75 80  
 Val Ile Gln Lys Gln Thr Phe Ile Ala Gln His Ala Cys Val Asn Ser  
 85 90 95  
 Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala  
 100 105 110  
 Gly Ile Ile Pro Leu Gly Asn Ser Ser Asn Gln Val Ser His Trp Asp  
 115 120 125  
 Leu Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly  
 130 135 140  
 Phe Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile  
 145 150 155 160  
 Ile Tyr Ala Leu Leu Gly Ile Pro Leu Glu Gly Phe Leu Leu Ala Gly  
 165 170 175  
 Val Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val  
 180 185 190  
 Glu Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile  
 195 200 205  
 Ile Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala  
 210 215 220  
 Leu Pro Ala Val Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp  
 225 230 235 240  
 Ala Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp  
 245 250 255  
 Tyr Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro  
 260 265 270  
 Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val  
 275 280 285  
 Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr Lys  
 290 295 300  
 Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn  
 305 310 315 320  
 Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile  
 325 330 335



<210> 12  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> TOK-1 P1

<400> 12  
Tyr Gly Asn Ala Leu Tyr Phe Cys Thr Val Ser Leu Leu Thr Val Gly  
1 5 10 15  
Leu Gly Asp Ile Leu Pro Lys Ser Val Gly Ala  
20 25

<210> 13  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> Slo

<400> 13  
Tyr Trp Thr Cys Val Tyr Phe Leu Ile Val Thr Met Ser Thr Val Gly  
1 5 10 15  
Tyr Gly Asp Val Tyr Cys Glu Thr Val Leu Gly  
20 25

<210> 14  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> Shaker

<400> 14  
Ile Pro Asp Ala Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly  
1 5 10 15  
Tyr Gly Asp Met Thr Pro Val Gly Phe Trp Gly  
20 25

<210> 15  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> Shab

<400> 15  
Ile Pro Glu Ala Phe Trp Trp Ala Gly Ile Thr Met Thr Thr Val Gly  
1 5 10 15  
Tyr Gly Asp Ile Cys Pro Thr Thr Ala Leu Gly  
20 25

<210> 16  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> Shal

<400> 16  
Ile Pro Ala Ala Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu Gly  
1 5 10 15  
Tyr Gly Asp Met Val Pro Glu Thr Ile Ala Gly  
20 25

<210> 17  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> Shaw

<400> 17  
Ile Pro Leu Gly Leu Trp Trp Ala Leu Val Thr Met Thr Thr Val Gly  
1 5 10 15  
Tyr Gly Asp Met Ala Pro Lys Thr Tyr Ile Gly  
20 25

<210> 18



<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> KAT1

<400> 18  
Tyr Val Thr Ala Leu Tyr Trp Ser Ile Thr Thr Leu Thr Thr Thr Gly  
1 5 10 15  
Tyr Gly Asp Phe His Ala Glu Asn Pro Arg Glu  
20 25

<210> 19  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> AKT1

<400> 19  
Tyr Val Thr Ser Met Tyr Trp Ser Ile Thr Thr Leu Thr Thr Val Gly  
1 5 10 15  
Tyr Gly Asp Ile His Pro Val Asn Thr Lys Glu  
20 25

<210> 20  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> eag

<400> 20  
Tyr Val Thr Ala Leu Tyr Phe Thr Met Thr Cys Met Thr Ser Val Gly  
1 5 10 15  
Phe Gly Asn Val Ala Ala Glu Thr Asp Asn Glu  
20 25

<210> 21  
<211> 27

<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K<sup>+</sup> channel sequence

<220>  
<223> ROMK1

<400> 21  
Met Thr Ser Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly  
1 5 10 15  
Tyr Gly Phe Arg Phe Val Thr Glu Gln Cys Ala  
20 25

<210> 22  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K<sup>+</sup> channel sequence

<220>  
<223> IRK1

<400> 22  
Phe Thr Ala Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly  
1 5 10 15  
Tyr Gly Phe Arg Cys Val Thr Asp Glu Cys Pro  
20 25

<210> 23  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K<sup>+</sup> channel sequence

<220>  
<223> GIRK1

<400> 23  
Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly  
1 5 10 15  
Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro  
20 25

<210> 24  
<211> 48  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: antisense  
oligonucleotide complementary to the partial  
mouse cDNA sequence of TASK

<400> 24

caccagcagg taggtgaagg tgcacacgat gagagccaac gtgcgcac

48

TGTCGCACGAGAGCCAACTGCACACGATGAGTGAAGGTAGGCAGCACC